

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:32:02 ; Search time 9 Seconds
(without alignments)
0.949 Million cell updates/eic

Title: US-10-825-958-13

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

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3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	32	US-09-731-889-6	Sequence 6, Appli
3	19	100.0	40	US-09-731-889-2	Sequence 2, Appli
4	19	100.0	40	US-09-731-889-5	Sequence 5, Appli
5	19	100.0	40	US-11-104-300-3	Sequence 3, Appli
6	19	100.0	42	US-09-731-889-3	Sequence 3, Appli
7	19	100.0	42	US-11-104-300-2	Sequence 4, Appli
8	19	100.0	43	US-09-731-889-4	Sequence 1, Appli
9	19	100.0	59	US-09-731-889-1	Sequence 49, Appli
10	19	100.0	71	US-11-254-185-19	Sequence 2, Appli
11	19	100.0	123	US-11-254-185-29	Sequence 49, Appli
12	19	100.0	148	US-10-196-749-456	Sequence 456, Appli
13	19	100.0	254	US-11-167-773-57	Sequence 76, Appli
14	19	100.0	254	US-11-167-773-76	Sequence 76, Appli
15	19	100.0	282	US-11-251-466-46	Sequence 46, Appli
16	19	100.0	282	US-11-254-784-12	Sequence 46, Appli
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18	19	100.0	313	US-09-949-925-89	Sequence 89, Appli
19	19	100.0	344	US-10-505-928-652	Sequence 652, Appli
20	19	100.0	424	US-10-196-749-8	Sequence 8, Appli
21	19	100.0	448	US-10-975-682-15	Sequence 15, Appli
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23	19	100.0	711	US-11-258-767-12	Sequence 12, Appli
24	19	100.0	711	US-11-258-767-15	Sequence 15, Appli
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30	19	100.0	711	US-11-258-767-34	Sequence 34, Appli
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33	19	100.0	1333	US-10-511-937-2992	Sequence 2992, Ap
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35	19	100.0	2871	US-10-505-928-100	Sequence 100, Ap
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38	18	94.7	267	US-11-024-545-63	Sequence 63, Appli
39	18	94.7	267	US-11-251-466-37	Sequence 37, Appli
40	18	94.7	267	US-11-254-173-48	Sequence 48, Appli
41	18	94.7	267	US-11-264-784-51	Sequence 51, Appli
42	18	94.7	344	US-10-196-749-178	Sequence 178, Ap
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44	18	94.7	363	US-10-511-937-2554	Sequence 2554, Ap
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46	18	94.7	378	US-10-511-937-2404	Sequence 2404, Ap
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48	18	94.7	544	US-10-505-928-859	Sequence 859, Ap
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55	18	94.7	1575	US-10-505-928-257	Sequence 257, Ap
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59	18	94.7	4074	US-10-501-834-2	Sequence 2, Appli
60	17	89.5	117	US-11-301-554-1673	Sequence 1673, Ap
61	17	89.5	145	US-11-301-554-1672	Sequence 1672, Ap
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71	16	84.2	13	US-11-264-509A-132	Sequence 132, Ap
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76	16	84.2	228	US-10-505-928-183	Sequence 183, Ap
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86	16	84.2	334	US-10-538-066-763	Sequence 763, Ap
87	16	84.2	374	US-10-511-937-2420	Sequence 2420, Ap
88	16	84.2	393	US-10-538-066-367	Sequence 367, Ap
89	16	84.2	393	US-11-315-777-9	Sequence 9, Appli
90	16	84.2	442	US-11-101-316-76	Sequence 76, Appli
91	16	84.2	446	US-10-505-928-833	Sequence 833, Appli
92	16	84.2	488	US-10-196-749-496	Sequence 496, Ap
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94	16	84.2	487	US-10-196-749-16	Sequence 16, Appli
95	16	84.2	487	US-11-242-111-27	Sequence 27, Appli
96	16	84.2	489	US-11-101-316-58	Sequence 58, Appli
97	16	84.2	490	US-10-982-908-18	Sequence 18, Appli
98	16	84.2	502	US-10-196-749-400	Sequence 400, Ap

99	16	84.2	502	7	US-11-311-555-12	Sequence 12, Appl	172	15	78.9	352	6	US-10-511-937-2412	Sequence 2412, Ap
100	16	84.2	502	7	US-11-311-561-12	Sequence 12, Appl	173	15	78.9	372	7	US-11-251-465-71	Sequence 71, Appl
101	16	84.2	502	7	US-11-101-316-158	Sequence 158, App	174	15	78.9	392	6	US-10-511-937-2583	Sequence 2583, Ap
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107	16	84.2	526	7	US-10-196-749-398	Sequence 398, App	180	15	78.9	457	7	US-11-101-316-12	Sequence 12, Appl
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110	16	84.2	737	6	US-10-505-928-123	Sequence 123, App	183	15	78.9	474	6	US-10-982-908-16	Sequence 16, Appl
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112	16	84.2	763	6	US-10-505-928-304	Sequence 304, App	185	15	78.9	475	6	US-10-982-908-12	Sequence 12, Appl
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115	16	84.2	820	6	US-10-982-908-26	Sequence 26, Appl	188	15	78.9	481	7	US-11-249-111-77	Sequence 77, Appl
116	16	84.2	821	6	US-10-505-928-316	Sequence 316, App	189	15	78.9	500	7	US-11-254-195-6	Sequence 6, Appl1
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120	16	84.2	967	6	US-10-505-928-795	Sequence 795, App	193	15	78.9	505	7	US-11-242-111-28	Sequence 28, Appl
121	16	84.2	995	7	US-11-246-999-48	Sequence 48, Appl	194	15	78.9	506	6	US-10-505-928-135	Sequence 135, App
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123	16	84.2	1185	6	US-10-511-937-3566	Sequence 3566, Ap	196	15	78.9	531	7	US-11-302-678-56	Sequence 56, Appl
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125	16	84.2	1539	6	US-10-511-937-2545	Sequence 2545, Ap	198	15	78.9	542	7	US-11-227-614-4	Sequence 4, Appl1
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127	16	84.2	1842	6	US-10-511-937-2929	Sequence 2929, App	200	15	78.9	557	6	US-10-511-937-2407	Sequence 2407, Ap
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129	16	84.2	2351	7	US-11-183-218-30	Sequence 30, Appl	202	15	78.9	648	6	US-10-511-814-14	Sequence 14, Appl
130	16	84.2	2351	7	US-11-280-757-35	Sequence 35, Appl	203	15	78.9	653	6	US-10-505-928-211	Sequence 211, App
131	16	84.2	4590	7	US-10-505-928-569	Sequence 569, App	204	15	78.9	654	7	US-11-302-678-26	Sequence 26, Appl
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134	15	78.9	9	6	US-10-538-066-422	Sequence 322, App	207	15	78.9	759	6	US-10-511-937-3015	Sequence 3015, App
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138	15	78.9	11	6	US-10-538-066-21	Sequence 21, Appl	211	15	78.9	825	6	US-10-511-937-3001	Sequence 3001, App
139	15	78.9	13	6	US-10-538-066-651	Sequence 651, App	212	15	78.9	847	6	US-10-505-928-330	Sequence 300, App
140	15	78.9	68	1	US-09-949-925-116	Sequence 116, App	213	15	78.9	1050	6	US-10-511-937-2573	Sequence 2573, App
141	15	78.9	69	6	US-10-982-908-22	Sequence 22, Appl	214	15	78.9	1032	6	US-10-497-088-21	Sequence 21, Appl
142	15	78.9	75	7	US-11-251-465-1	Sequence 1, Appl1	215	15	78.9	1342	6	US-10-497-088-14	Sequence 14, Appl
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147	15	78.9	152	7	US-11-301-554-787	Sequence 787, App	220	14	73.7	9	7	US-11-140-487A-2095	Sequence 2095, Ap
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149	15	78.9	164	6	US-10-505-928-706	Sequence 706, App	222	14	73.7	10	6	US-11-140-487A-880	Sequence 880, App
150	15	78.9	164	6	US-10-511-814-4	Sequence 4, Appl1	223	14	73.7	10	7	US-11-140-487A-1018	Sequence 1018, App
151	15	78.9	164	6	US-11-242-111-26	Sequence 26, Appl	224	14	73.7	10	7	US-11-140-487A-1728	Sequence 1728, Ap
152	15	78.9	166	6	US-10-538-066-761	Sequence 761, App	225	14	73.7	15	6	US-10-370-959-125	Sequence 125, App
153	15	78.9	197	6	US-10-511-937-2611	Sequence 2611, App	226	14	73.7	20	7	US-11-301-554-2103	Sequence 2103, Ap
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156	15	78.9	197	7	US-11-311-561-4	Sequence 4, Appl1	229	14	73.7	23	7	US-11-251-465-124	Sequence 124, App
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159	15	78.9	251	7	US-11-249-111-111	Sequence 111, Appl	232	14	73.7	43	1	US-09-949-925-129	Sequence 129, App
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162	15	78.9	313	6	US-11-257-062-48	Sequence 48, Appl	235	14	73.7	52	7	US-11-324-517-21	Sequence 21, Appl
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167	15	78.9	331	7	US-11-024-545-3	Sequence 2, Appl1	240	14	73.7	81	6	US-10-525-126-209	Sequence 209, App
168	15	78.9	331	7	US-11-190-750-30	Sequence 30, Appl	241	14	73.7	81	6	US-10-525-126-210	Sequence 210, App
169	15	78.9	345	7	US-11-264-784-96	Sequence 96, Appl	242	14	73.7	81	6	US-10-525-126-211	Sequence 211, App
170	15	78.9	345	7	US-11-249-111-65	Sequence 65, Appl	243	14	73.7	81	6	US-10-525-126-240	Sequence 240, App
171	15	78.9	350	6	US-10-511-937-2609	Sequence 2609, Ap	244	14	73.7	81	6	US-10-525-126-241	Sequence 241, App

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:20:21 ; Search time 196 Seconds

(without alignments)
9.331 Million cell updates/sec

Title: US-10-825-958-13

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	2	AAW45956 Amyloid b
2	19	100.0	4	3	AAV79936 Beta-amy1
3	19	100.0	4	4	AAW48487 Anti-fibr1
4	19	100.0	4	4	AAW48479 Anti-fibr1
5	19	100.0	4	4	AAW82635 All-D pep
6	19	100.0	4	4	AAW82627 All-D pep
7	19	100.0	4	4	AAW96815 Amyloid t
8	19	100.0	4	5	AAU96823 Amyloid t
9	19	100.0	4	5	AAU11661 Peptide #
10	19	100.0	4	5	AAU11653 Peptide #
11	19	100.0	4	6	AAE35442 Abeta pep
12	19	100.0	4	6	AAE35449 Abeta pep
13	19	100.0	4	6	AAO37266 Vaccine a
14	19	100.0	4	8	AAO37284 Amyloid-b
15	19	100.0	4	8	AAO37326 Anti-fibr1
16	19	100.0	4	8	AAO37318 Anti-fibr1
17	19	100.0	4	9	AAO37274 Vaccine a
18	19	100.0	4	9	AAO37295 Amyloid-t
19	19	100.0	4	9	AAO37933 Amyloid-t
20	19	100.0	4	9	AAW23038 Human Abe
21	19	100.0	5	2	AAW87922 Test pep
22	19	100.0	5	2	AAW02315 Beta-amy1
23	19	100.0	5	2	AAW45933 Partial s

24	19	100.0	5	2	AAW45966
25	19	100.0	5	2	AAW45950
26	19	100.0	5	2	AAW29089
27	19	100.0	5	2	AAW89367
28	19	100.0	5	3	AAV79937
29	19	100.0	5	4	AAW67279
30	19	100.0	5	4	AAW48489
31	19	100.0	5	4	AAW48481
32	19	100.0	5	4	AAW82637
33	19	100.0	5	4	AAW82629
34	19	100.0	5	4	AAW62803
35	19	100.0	5	5	AAW71010
36	19	100.0	5	5	AAO15847
37	19	100.0	5	5	AAW05183
38	19	100.0	5	5	AAW05158
39	19	100.0	5	5	AAW96825
40	19	100.0	5	5	AAU96817
41	19	100.0	5	5	AAW84001
42	19	100.0	5	5	AAU11655
43	19	100.0	5	5	AAU11663
44	19	100.0	5	6	AAW82632
45	19	100.0	5	6	AAE35444
46	19	100.0	5	6	AAE35451
47	19	100.0	5	6	AAW43903
48	19	100.0	5	7	ADP60931
49	19	100.0	5	8	ADJ71329
50	19	100.0	5	8	ADJ64061
51	19	100.0	5	8	ADJ64088
52	19	100.0	5	8	ADW97741
53	19	100.0	5	8	ADP64923
54	19	100.0	5	8	ADQ37328
55	19	100.0	5	8	ADQ37276
56	19	100.0	5	8	ADQ37354
57	19	100.0	5	8	ADQ37268
58	19	100.0	5	8	ADQ37320
59	19	100.0	5	8	ADQ37342
60	19	100.0	5	8	ADQ37382
61	19	100.0	5	9	ADY37927
62	19	100.0	5	9	ADY37935
63	19	100.0	5	9	ADZ59195
64	19	100.0	5	9	AEA23037
65	19	100.0	5	9	AEA28520
66	19	100.0	5	10	AAE64847
67	19	100.0	6	2	AAW02331
68	19	100.0	6	2	AAW02313
69	19	100.0	6	2	AAW02314
70	19	100.0	6	2	AAW45945
71	19	100.0	6	2	AAW45944
72	19	100.0	6	2	AAW29092
73	19	100.0	6	2	AAW29091
74	19	100.0	6	2	AAW29090
75	19	100.0	6	2	AAW89378
76	19	100.0	6	2	AAW89377
77	19	100.0	6	2	AAW89388
78	19	100.0	6	4	AAW48476
79	19	100.0	6	4	AAW48474
80	19	100.0	6	4	AAW48496
81	19	100.0	6	4	AAW82654
82	19	100.0	6	4	AAW82657
83	19	100.0	6	4	AAW82660
84	19	100.0	6	4	AAW82663
85	19	100.0	6	4	AAW82651
86	19	100.0	6	4	AAW82632
87	19	100.0	6	5	ABG71031
88	19	100.0	6	5	ABG71009
89	19	100.0	6	5	ABG71008
90	19	100.0	6	5	ABW05177
91	19	100.0	6	5	ABW05156
92	19	100.0	6	5	ABW05157
93	19	100.0	6	5	ABW05189
94	19	100.0	6	5	AAU96820
95	19	100.0	6	5	AAW83305
96	19	100.0	6	5	AAU11658

AAW45966	Peptide d
AAW45950	Amyloid b
AAW29089	A-beta-bi
AAW89367	Beta-amy1
AAV79937	Beta-amy1
AAW67279	Residues
AAW48489	Anti-fibr1
AAW48481	Anti-fibr1
AAW82637	All-D pep
AAW82629	All-D pep
AAW62803	Residues
AAW71010	Long form
AAO15847	Beta-amy1
AAW05183	Beta amy1
AAW05158	Beta amy1
AAU96825	Amyloid t
AAU96817	Amyloid t
AAW84001	Transglut
AAU11655	Peptide #
AAU11663	Peptide #
AAW82632	Abeta fib
AAE35444	Abeta pep
AAE35451	Abeta pep
AAW43903	C-termina
ADP60931	Pathologi
ADJ71329	Human bet
ADJ64061	Human bet
ADJ64088	Human bet
ADW97741	Amyloid b
ADP64923	Beta-amy1
ADQ37328	Anti-fibr1
ADQ37276	Vaccine a
ADQ37354	Beta-amy1
ADQ37268	Vaccine a
ADQ37320	Anti-fibr1
ADQ37342	Amyloid-b
ADQ37382	Amyloid-b
ADY37927	Amyloid-t
ADY37935	Amyloid-t
ADZ59195	Human amy
AEA23037	Human amy
AEA28520	Short amy
AAE64847	A alpha f
AAW02331	Beta-amy1
AAW02313	Beta-amy1
AAW02314	Beta-amy1
AAW45945	Amyloid b
AAW45944	Amyloid b
AAW29092	A-beta-bi
AAW29091	A-beta-bi
AAW29090	A-beta-bi
AAW89378	Beta-amy1
AAW89377	Beta-amy1
AAW89388	Beta-amy1
AAW48476	Anti-fibr1
AAW48474	Anti-fibr1
AAW48496	Anti-fibr1
AAW82654	All-D pep
AAW82657	All-D pep
AAW82660	All-D pep
AAW82663	All-D pep
AAW82651	All-D pep
AAW82632	All-D pep
ABG71031	Long form
ABG71009	Long form
ABG71008	Long form
ABW05177	Beta amy1
ABW05156	Beta amy1
ABW05157	Beta amy1
ABW05189	Beta amy1
AAU96820	Amyloid t
AAW83305	Amyloid-b
AAU11658	Peptide #

97.	19	100.0	6	5	AU11911	Peptide #	170	19	100.0	7	7	ADD20746	ADD20746 Human bet
98	19	100.0	6	5	AU11650	Peptide #	171	19	100.0	7	7	ADP50855	ADP50855 Human cal
99	19	100.0	6	6	AAE35476	Abeta pep	172	19	100.0	7	7	ADP64057	ADP64057 Human bet
100	19	100.0	6	6	AAE35470	Abeta pep	173	19	100.0	7	8	ADP64058	ADP64058 Human bet
101	19	100.0	6	6	AAE35482	Abeta pep	174	19	100.0	7	8	ADP64922	ADP64922 Beta-amy1
102	19	100.0	6	6	AAE35445	Abeta pep	175	19	100.0	7	8	ADP637378	ADP637378 Amyloid-b
103	19	100.0	6	6	AAE35473	Abeta pep	176	19	100.0	7	8	ADP37278	ADP37278 Vaccine a
104	19	100.0	6	6	AAE35479	Abeta pep	177	19	100.0	7	8	ADP37350	ADP37350 Beta-amy1
105	19	100.0	6	6	AAE35434	Abeta pep	178	19	100.0	7	8	ADP37379	ADP37379 Amyloid-b
106	19	100.0	6	6	ADP64060	Human bet	179	19	100.0	7	8	ADP37314	ADP37314 Antifibril
107	19	100.0	6	8	ADP64059	Human bet	180	19	100.0	7	8	ADP37263	ADP37263 Vaccine a
108	19	100.0	6	8	ADP64094	Human bet	181	19	100.0	7	8	ADP37279	ADP37279 Vaccine a
109	19	100.0	6	8	ADP64082	Human bet	182	19	100.0	7	8	ADP37330	ADP37330 Antifibril
110	19	100.0	6	8	ADP37300	Vaccine a	183	19	100.0	7	8	ADP37331	ADP37331 Antifibril
111	19	100.0	6	8	ADP37271	Vaccine a	184	19	100.0	7	8	ADP37351	ADP37351 Beta-amy1
112	19	100.0	6	8	ADP37380	Amyloid-b	185	19	100.0	7	9	ADP37922	ADP37922 Amyloid-c
113	19	100.0	6	8	ADP37315	Antifibril	186	19	100.0	7	9	ADP37938	ADP37938 Amyloid-c
114	19	100.0	6	8	ADP37335	Antifibril	187	19	100.0	7	9	ADP37937	ADP37937 Amyloid-c
115	19	100.0	6	8	ADP37368	Beta-amy1	188	19	100.0	7	9	ADP37937	ADP37937 Amyloid-c
116	19	100.0	6	8	ADP37306	Vaccine a	189	19	100.0	8	2	AAE74105	AAE74105 P-selectin
117	19	100.0	6	8	ADP37297	Vaccine a	190	19	100.0	8	2	AAE74104	AAE74104 P-selectin
118	19	100.0	6	8	ADP37269	Vaccine a	191	19	100.0	8	2	AAE74099	AAE74099 P-selectin
119	19	100.0	6	8	ADP37303	Vaccine a	192	19	100.0	8	2	AAE74099	AAE74099 P-selectin
120	19	100.0	6	8	ADP37352	Beta-amy1	193	19	100.0	8	2	AAE74099	AAE74099 P-selectin
121	19	100.0	6	8	ADP37292	Vaccine a	194	19	100.0	8	2	AAE74099	AAE74099 P-selectin
122	19	100.0	6	8	ADP37381	Amyloid-b	195	19	100.0	8	2	AAE74099	AAE74099 P-selectin
123	19	100.0	6	8	ADP37258	Vaccine a	196	19	100.0	8	2	AAE74099	AAE74099 P-selectin
124	19	100.0	6	8	ADP37294	Vaccine a	197	19	100.0	8	2	AAE74099	AAE74099 P-selectin
125	19	100.0	6	8	ADP37353	Beta-amy1	198	19	100.0	8	4	AAE10663	AAE10663 Human amy
126	19	100.0	6	8	ADP37323	Antifibril	199	19	100.0	8	4	AAE10663	AAE10663 Human amy
127	19	100.0	6	8	ADP37370	Amyloid-b	200	19	100.0	8	5	ABG71005	ABG71005 Long form
128	19	100.0	6	9	ADP37348	Amyloid-c	201	19	100.0	8	5	ABG71005	ABG71005 Long form
129	19	100.0	6	9	ADP37330	Test pep	202	19	100.0	8	5	ABG71005	ABG71005 Long form
130	19	100.0	6	9	ADP37348	Amyloid-c	203	19	100.0	8	5	ABG71005	ABG71005 Long form
131	19	100.0	6	9	ADP37348	Amyloid-c	204	19	100.0	8	5	ABG71005	ABG71005 Long form
132	19	100.0	6	9	ADP37348	Amyloid-c	205	19	100.0	8	6	ABG71005	ABG71005 Long form
133	19	100.0	6	9	ADP37348	Amyloid-c	206	19	100.0	8	7	ABG71005	ABG71005 Long form
134	19	100.0	6	9	ADP37348	Amyloid-c	207	19	100.0	8	8	ADP37377	ADP37377 Amyloid-b
135	19	100.0	6	9	ADP37348	Amyloid-c	208	19	100.0	8	8	ADP37385	ADP37385 Antifibril
136	19	100.0	6	9	ADP37348	Amyloid-c	209	19	100.0	8	8	ADP37349	ADP37349 Beta-amy1
137	19	100.0	6	9	ADP37348	Amyloid-c	210	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
138	19	100.0	6	9	ADP37348	Amyloid-c	211	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
139	19	100.0	6	9	ADP37348	Amyloid-c	212	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
140	19	100.0	6	9	ADP37348	Amyloid-c	213	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
141	19	100.0	6	9	ADP37348	Amyloid-c	214	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
142	19	100.0	6	9	ADP37348	Amyloid-c	215	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
143	19	100.0	6	9	ADP37348	Amyloid-c	216	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
144	19	100.0	6	9	ADP37348	Amyloid-c	217	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
145	19	100.0	6	9	ADP37348	Amyloid-c	218	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
146	19	100.0	6	9	ADP37348	Amyloid-c	219	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
147	19	100.0	6	9	ADP37348	Amyloid-c	220	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
148	19	100.0	6	9	ADP37348	Amyloid-c	221	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
149	19	100.0	6	9	ADP37348	Amyloid-c	222	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
150	19	100.0	6	9	ADP37348	Amyloid-c	223	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
151	19	100.0	6	9	ADP37348	Amyloid-c	224	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
152	19	100.0	6	9	ADP37348	Amyloid-c	225	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
153	19	100.0	6	9	ADP37348	Amyloid-c	226	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
154	19	100.0	6	9	ADP37348	Amyloid-c	227	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
155	19	100.0	6	9	ADP37348	Amyloid-c	228	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
156	19	100.0	6	9	ADP37348	Amyloid-c	229	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
157	19	100.0	6	9	ADP37348	Amyloid-c	230	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
158	19	100.0	6	9	ADP37348	Amyloid-c	231	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
159	19	100.0	6	9	ADP37348	Amyloid-c	232	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
160	19	100.0	6	9	ADP37348	Amyloid-c	233	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
161	19	100.0	6	9	ADP37348	Amyloid-c	234	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
162	19	100.0	6	9	ADP37348	Amyloid-c	235	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
163	19	100.0	6	9	ADP37348	Amyloid-c	236	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
164	19	100.0	6	9	ADP37348	Amyloid-c	237	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
165	19	100.0	6	9	ADP37348	Amyloid-c	238	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
166	19	100.0	6	9	ADP37348	Amyloid-c	239	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
167	19	100.0	6	9	ADP37348	Amyloid-c	240	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
168	19	100.0	6	9	ADP37348	Amyloid-c	241	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1
169	19	100.0	6	9	ADP37348	Amyloid-c	242	19	100.0	8	9	ADP37349	ADP37349 Beta-amy1

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:20:33 ; Search time 297 Seconds
(Without alignments)
12.458 Million cell updates/sec

Title: US-10-825-958-13
Perfect score: 19
Sequence: 1 KLVF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	14	2	Q8IM66_HUMAN
2	19	100.0	14	2	Q9UH91_HUMAN
3	19	100.0	19	2	Q4XV14_PLACH
4	19	100.0	19	2	Q692Y3_SOYBN
5	19	100.0	27	2	Q9UW68_9EURY
6	19	100.0	28	2	Q4N1Z6_THERP
7	19	100.0	28	2	Q7RAW5_PLA80
8	19	100.0	28	2	Q7RNI4_PLA80
9	19	100.0	29	2	Q4RDS4_TETNG
10	19	100.0	31	2	Q7R9H4_PLA80
11	19	100.0	31	2	Q47XC8_COLP3
12	19	100.0	33	2	Q9UC33_HUMAN
13	19	100.0	35	2	Q4X2D2_PLACH
14	19	100.0	38	2	Q4YA98_PLA80
15	19	100.0	39	2	Q7Z988_SCHPO
16	19	100.0	39	2	Q7RSM3_PLA80
17	19	100.0	39	2	Q8BGU3_MOUSE
18	19	100.0	41	2	Q4YAX8_PLA80
19	19	100.0	41	2	Q8KEH6_CHLRE
20	19	100.0	42	2	Q561U6_GRA8R
21	19	100.0	42	2	Q561U7_TURTR
22	19	100.0	42	2	Q7M088_CAVPO
23	19	100.0	42	2	Q8AXZ2_ICRPU
24	19	100.0	43	2	Q3VNU9_9CHLB
25	19	100.0	44	2	Q4YIHS_PLACH
26	19	100.0	44	2	Q856G0_9CAUD
27	19	100.0	45	2	Q72ZB2_BACCI
28	19	100.0	47	2	Q524S5_9EURY
29	19	100.0	48	2	Q54MK0_DICDI
30	19	100.0	48	2	Q9GR26_APHCO
31	19	100.0	50	2	Q3DGO1_STRAG

32	19	100.0	50	2	Q3XXS7_ENTFC	Q3XXS7 enterococc
33	19	100.0	51	2	Q4Y6Z7_PLACH	Q4Y6Z7 plasmodium
34	19	100.0	51	2	Q4VKD5_9EURY	Q4VKD5 meganactiph
35	19	100.0	51	2	Q4VKF3_9EURY	Q4VKF3 meganactiph
36	19	100.0	51	2	Q72A51_DESVH	Q72A51 desulfobib
37	19	100.0	51	2	Q8QMN2_COMFV	Q8QMN2 cowpox viru
38	19	100.0	52	2	Q8WZ99_HUMAN	Q8WZ99 homo sapien
39	19	100.0	52	2	Q7RGM2_PLA80	Q7RGM2 plasmodium
40	19	100.0	52	2	Q9MEH0_9EURY	Q9MEH0 meganactiph
41	19	100.0	53	2	Q7MIN5_SOYBN	Q7MIN5 glycine max
42	19	100.0	53	2	Q2SMU7_9GAMM	Q2SMU7 habella che
43	19	100.0	53	2	Q5XXM2_RICCN	Q5XXM2 rickettsia
44	19	100.0	54	2	Q4X433_PLACH	Q4X433 plasmodium
45	19	100.0	54	2	Q8R8V2_THERN	Q8R8V2 thermoaer
46	19	100.0	56	2	Q5HDA2_STAAC	Q5HDA2 staphylococ
47	19	100.0	57	1	A4_URSTA	Q29149 u amyloid b
48	19	100.0	57	2	Q7UFC9_RHOBA	Q7UFC9 rhodospirell
49	19	100.0	57	2	Q921T0_RICCN	Q921T0 rickettsia
50	19	100.0	58	1	A4_CANFA	Q28280 c amyloid b
51	19	100.0	58	1	A4_RABIT	Q28757 o amyloid b
52	19	100.0	58	1	A3_SHEEP	Q39653 small round
53	19	100.0	58	1	Q35633_9CALI	Q28053 b amyloid b
54	19	100.0	59	1	A4_BOVIN	Q2H2E1 capra nubia
55	19	100.0	59	2	Q2H2T1_CAPNU	Q2H2E1 capra nubia
56	19	100.0	59	2	Q4T197_TETNG	Q4T197 tetradon n
57	19	100.0	60	2	Q8KYD1_BACAN	Q8KYD1 bacillus an
58	19	100.0	60	2	Q6F0Z5_BACAN	Q6F0Z5 bacillus an
59	19	100.0	60	2	Q4RUF7_TETNG	Q4RUF7 tetradon n
60	19	100.0	61	2	Q3ISR5_SHIBS	Q3ISR5 shigella bo
61	19	100.0	61	2	Q3YTD0_SHISS	Q3YTD0 shigella so
62	19	100.0	61	2	Q3YTX7_SHISS	Q3YTX7 shigella so
63	19	100.0	61	2	Q2NKO3_9MOIU	Q2NKO3 aster yell
64	19	100.0	61	2	Q9AFZ0_SHIFL	Q9AFZ0 shigella fl
65	19	100.0	62	2	Q4YEM0_PLA80	Q4YEM0 plasmodium
66	19	100.0	62	2	Q2H2T8_CAPII	Q2H2T8 capra ibex
67	19	100.0	62	2	Q8W6C9_9VIRU	Q8W6C9 vibrio phag
68	19	100.0	62	2	Q30ZAB_STRSU	Q30ZAB streptococ
69	19	100.0	62	2	Q8E113_STRAS	Q8E113 streptococ
70	19	100.0	62	2	Q51CQ6_GADEN	Q51CQ6 human adeno
71	19	100.0	63	2	Q8EBJ7_PIG	Q8EBJ7 sus scrofa
72	19	100.0	63	2	Q598Z9_BALBO	Q598Z9 balenopter
73	19	100.0	64	2	Q59NH7_DROME	Q59NH7 drosophila
74	19	100.0	64	2	Q3MQZ5_ANTST	Q3MQZ5 antechinus
75	19	100.0	64	2	Q3B457_PELLD	Q3B457 pelodicyon
76	19	100.0	64	2	Q43GCI_9CHLB	Q43GCI chlorobium
77	19	100.0	64	2	Q720Z9_TEBIC	Q720Z9 leprospira
78	19	100.0	64	2	Q8F4T7_LEBIN	Q8F4T7 leprospira
79	19	100.0	65	2	Q94144_CABEL	Q94144 caenorhabd
80	19	100.0	65	2	Q4TE84_TETNG	Q4TE84 tetradon n
81	19	100.0	66	2	Q2H2S1_9CETA	Q2H2S1 capra pyren
82	19	100.0	66	2	Q2H2S2_CAPSI	Q2H2S2 capra sibir
83	19	100.0	66	2	Q2H2S7_CAPSI	Q2H2S7 capra sibir
84	19	100.0	66	2	Q2H2T7_CAPNU	Q2H2T7 capra nubia
85	19	100.0	66	2	Q2H2T9_CAPII	Q2H2T9 capra ibex
86	19	100.0	66	2	Q2H2U1_CAPCY	Q2H2U1 capra cylin
87	19	100.0	66	2	Q2H2U2_CAPCU	Q2H2U2 capra cauca
88	19	100.0	66	2	Q2H2U4_CAPCU	Q2H2U4 capra cauca
89	19	100.0	66	2	Q858S3_9VIRU	Q858S3 bacterioph
90	19	100.0	66	2	Q6F8Q6_ACTAD	Q6F8Q6 actinobact
91	19	100.0	66	2	Q8BDT17_STRMU	Q8BDT17 streptococ
92	19	100.0	67	2	Q3PYM6_NITRA	Q3PYM6 nitroba
93	19	100.0	67	2	Q5L2M7_GEOXA	Q5L2M7 geobacillus
94	19	100.0	67	2	Q921F4_RICCN	Q921F4 rickettsia
95	19	100.0	67	2	Q7OHU9_PPRXA	Q7OHU9 pseudorab
96	19	100.0	68	2	Q7RAM0_PLA80	Q7RAM0 plasmodium
97	19	100.0	68	2	Q6Z0U8_ORYSA	Q6Z0U8 oryza sativ
98	19	100.0	69	1	Q61G3_ARATH	Q61G3 arabidopsi
99	19	100.0	69	2	Q4Q9Z2_LEBMA	Q4Q9Z2 leishmania
100	19	100.0	70	2	Q4XND3_PLACH	Q4XND3 plasmodium
101	19	100.0	70	2	Q6HNO3_BACHK	Q6HNO3 bacillus th
102	19	100.0	71	2	Q4A9T5_MYCHJ	Q4A9T5 mycoplasma
103	19	100.0	71	2	Q3UTF7_BURFI	Q3UTF7 burholderi
104	19	100.0	71	2	Q5F7S4_NEIG1	Q5F7S4 neisseria g

105	19	100.0	71	2	063TA0_BURPS	063ta0 burkholderi	178	19	100.0	81	2	08KX00_CHLITE	08kx00 chlorobium
106	19	100.0	71	2	08UCR6_AGRRT	08ucr6 agrobacteri	179	19	100.0	82	2	08HNX3_SHEMT	08hnx3 dactylopha
107	19	100.0	72	2	06CDK3_YARLT	06cdk3 yarrowia li	180	19	100.0	82	2	08KJX3_PROVU	08kjx3 proteus vul
108	19	100.0	72	2	025925_PLAFA	025925 plasmidium	181	19	100.0	82	2	05ICR2_ADE31	05icr2 human adeno
109	19	100.0	73	2	07P9F5_RICSI	07p9f5 rickettsia	182	19	100.0	82	2	05ICT4_ADE09	05ict4 human adeno
110	19	100.0	73	2	07MV83_PORGI	07mv83 porphyromon	183	19	100.0	82	2	05ICU0_ADE09	05icu0 human adeno
111	19	100.0	73	2	05ICP4_GADEN	05icp4 human adeno	184	19	100.0	83	2	04XBH3_PLACH	04xbh3 plasmidium
112	19	100.0	73	2	05ICR6_GADEN	05icr6 human adeno	185	19	100.0	83	2	04YDE2_PLABE	04yde2 plasmidium
113	19	100.0	73	2	05ICR7_GADEN	05icr7 human adeno	186	19	100.0	83	2	07R7E5_PLAYO	07r7e5 plasmidium
114	19	100.0	74	2	0461Q9_DROWI	0461q9 drosophila	187	19	100.0	83	2	02LGH3_MAIZE	02lgh3 zea mays (m
115	19	100.0	74	2	05CJH6_CRYHO	05cjh6 cryptospori	188	19	100.0	83	2	02LGH4_SERIT	02lgh4 setaria ita
116	19	100.0	74	2	0936G7_STAUP	0936g7 staphylococ	189	19	100.0	83	2	02LGH5_PENAM	02lgh5 penicillium
117	19	100.0	74	2	05B0S7_GADEN	05b0s7 staphylococ	190	19	100.0	83	2	02LGH6_SORHL	02lgh6 sorghum hal
118	19	100.0	74	2	05ICP5_GADEN	05icp5 human adeno	191	19	100.0	83	2	02LGH7_PANMI	02lgh7 panicum mil
119	19	100.0	74	2	05ICR7_ADE16	05icr7 human adeno	192	19	100.0	83	2	08UC93_AGRRT	08uc93 agrobacteri
120	19	100.0	75	2	081UQ0_BACAN	081uq0 bacillus an	193	19	100.0	83	2	05ICR4_GADEN	05icr4 human adeno
121	19	100.0	75	2	05B0G0_GADEN	05b0g0 untyped hum	194	19	100.0	83	2	05ICT5_ADE08	05ict5 human adeno
122	19	100.0	75	2	05B0G2_GADEN	05b0g2 untyped hum	195	19	100.0	84	2	074N49_NANEO	074n49 nanorarchaeu
123	19	100.0	75	2	05ICP9_GADEN	05icp9 human adeno	196	19	100.0	84	2	03C8K9_9CILOT	03c8k9 alkaliiphilu
124	19	100.0	75	2	05ICQ7_GADEN	05icq7 human adeno	197	19	100.0	84	2	082WG5_NITRU	082wg5 nitrosomonas
125	19	100.0	76	2	0592V4_LYMST	0592v4 lymanea sta	198	19	100.0	84	2	08YH11_BRUME	08yh11 brucella me
126	19	100.0	76	2	08VVM4_ECOLI	08vvm4 escherichia	199	19	100.0	84	2	05ICR5_GADEN	05icr5 human adeno
127	19	100.0	76	2	05B0S2_GADEN	05b0s2 untyped hum	200	19	100.0	84	2	05ICT9_ADE04	05ict9 human adeno
128	19	100.0	76	2	05B0S9_GADEN	05b0s9 untyped hum	201	19	100.0	85	2	05BR10_SCHJA	05br10 schistosoma
129	19	100.0	76	2	05ICP3_GADEN	05icp3 human adeno	202	19	100.0	85	2	032EP0_SHIDS	032ep0 shigella dy
130	19	100.0	76	2	05ICR0_GADEN	05icr0 human adeno	203	19	100.0	85	2	03ENN2_BACTI	03enn2 bacillus th
131	19	100.0	76	2	09TBS2_TOXRU	09tbs2 toxostoma r	204	19	100.0	85	2	08GJL9_SYMP7	08gj19 synecchococ
132	19	100.0	76	2	09TBS6_PPASS	09tbs6 toxostoma l	205	19	100.0	85	2	05MZR4_SYMP6	05mzr4 synecchococ
133	19	100.0	77	2	054879_STRPN	054879 streptococ	206	19	100.0	85	2	09BAC8_RHILLO	09bac8 rhizobium l
134	19	100.0	77	2	05B048_GADEN	05b048 untyped hum	207	19	100.0	85	2	05ICQ1_GADEN	05icq1 human adeno
135	19	100.0	77	2	05B0S5_GADEN	05b0s5 untyped hum	208	19	100.0	85	2	05ICR9_GADEN	05icr9 human adeno
136	19	100.0	77	2	05B0G4_GADEN	05b0g4 untyped hum	209	19	100.0	85	2	09TBO6_PPASS	09tbo6 toxostoma l
137	19	100.0	77	2	05ICP2_GADEN	05icp2 human adeno	210	19	100.0	85	2	09TBO7_PPASS	09tbo7 toxostoma l
138	19	100.0	77	2	05ICP7_GADEN	05icp7 human adeno	211	19	100.0	85	2	09TBO8_PPASS	09tbo8 toxostoma l
139	19	100.0	77	2	05ICP8_GADEN	05icp8 human adeno	212	19	100.0	85	2	09TBO9_PPASS	09tbo9 toxostoma b
140	19	100.0	77	2	05ICQ0_GADEN	05icq0 human adeno	213	19	100.0	85	2	09TBR2_9PASS	09tbr2 oreoscoptes
141	19	100.0	77	2	05ICQ4_GADEN	05icq4 human adeno	214	19	100.0	85	2	09TBR4_9PASS	09tbr4 oreoscoptes
142	19	100.0	77	2	05ICR1_GADEN	05icr1 human adeno	215	19	100.0	85	2	09TBR6_PPASS	09tbr6 toxostoma c
143	19	100.0	77	2	05ICR8_GADEN	05icr8 human adeno	216	19	100.0	85	2	09TBR8_PPASS	09tbr8 toxostoma c
144	19	100.0	77	2	05ICG1_GADEN	05icg1 human adeno	217	19	100.0	85	2	09TBS0_PPASS	09tbs0 toxostoma c
145	19	100.0	77	2	05ICG3_GADEN	05icg3 human adeno	218	19	100.0	85	2	09TBS4_TOXGU	09tbs4 toxostoma g
146	19	100.0	77	2	05ICG6_ADE17	05icg6 human adeno	219	19	100.0	86	1	RL23_METUA	RL23 metanococ
147	19	100.0	77	2	05ICR3_GADEN	05icr3 human adeno	220	19	100.0	86	2	03I1I6_PSEMT	03i1i6 pseudocalter
148	19	100.0	78	2	09HPR1_HALSA	09hpr1 halobacteri	221	19	100.0	86	2	043ITH_SOLUS	043ith solibacter
149	19	100.0	78	2	06BXN0_DBRHA	06bxn0 debaryomyce	222	19	100.0	87	2	04MPY6_ASPEU	04mpy6 aspergillus
150	19	100.0	78	2	06ICG5_DROME	06icg5 drosophila	223	19	100.0	87	2	08IGC2_DROME	08igc2 drosophila
151	19	100.0	78	2	03Y5V2_CITLA	03y5v2 citrullus l	224	19	100.0	87	2	03CYJ4_STRAG	03cyj4 streptococ
152	19	100.0	78	2	05B0S6_GADEN	05b0s6 untyped hum	225	19	100.0	87	2	03DQP5_STRAG	03dqp5 streptococ
153	19	100.0	78	2	05ICG8_ADE35	05icg8 human adeno	226	19	100.0	87	2	05ICT6_ADE07	05ict6 human adeno
154	19	100.0	78	2	05ICG5_ADE18	05icg5 human adeno	227	19	100.0	88	2	06LGG9_PHOPR	06lgg9 photobacter
155	19	100.0	78	2	05ICG8_ADE15	05icg8 human adeno	228	19	100.0	88	2	03US56_MOUSE	03us56 mus musculu
156	19	100.0	78	2	05ICR1_ADE12	05icr1 human adeno	229	19	100.0	89	2	03SAR6_9EURY	03sar6 uncultured
157	19	100.0	79	2	0969F3_HUMAN	0969f3 homo sapien	230	19	100.0	89	2	03SEBL5_DICDI	03sebl5 dictyostell
158	19	100.0	79	2	0711O2_IACDL	0711o2 lactobacilli	231	19	100.0	89	2	087BR3_STRP3	087br3 streptococ
159	19	100.0	79	2	05HMR0_STAEO	05hmr0 staphylococ	232	19	100.0	89	2	06MDW2_PARUM	06mdw2 paracitlamyd
160	19	100.0	79	2	081YZ4_BACAN	081yz4 bacillus an	233	19	100.0	90	2	09HMB9_HALSA	09hmb9 halobacteri
161	19	100.0	79	2	092GT7_RICCN	092gt7 rickettsia	234	19	100.0	90	2	053R27_HUMAN	053r27 homo sapien
162	19	100.0	79	2	0354G3_CRIGR	0354g3 cricetus	235	19	100.0	90	2	05XN00_MANES	05xn00 manihot ecc
163	19	100.0	79	2	05BQ51_GADEN	05bq51 untyped hum	236	19	100.0	90	2	03RGP8_XYUFA	03rgp8 xyella fab
164	19	100.0	79	2	05ICQ9_GADEN	05icq9 human adeno	237	19	100.0	90	2	03Y3G3_ENTFC	03y3g3 enterococcu
165	19	100.0	79	2	05ICG2_GADEN	05icg2 human adeno	238	19	100.0	90	2	09FP74_XYUFA	09fp74 xyella fab
166	19	100.0	80	2	05BSG2_SCHJA	05bsg2 schistosoma	239	19	100.0	90	2	09BAC5_PPASS	09bac5 nitrosomonas
167	19	100.0	80	2	02SLP8_SGAMW	02slp8 habella che	240	19	100.0	91	1	SPC1_ASHOO	SPC1 ashbya goss
168	19	100.0	80	2	03Y0Z0_ENTFC	03y0z0 enterococcu	241	19	100.0	91	1	Y909_METUA	Y909 metanococ
169	19	100.0	80	2	063R33_BACC2	063r33 bacillus ce	242	19	100.0	91	2	064PX0_BACFR	064px0 bacteroides
170	19	100.0	80	2	05ICP6_GADEN	05icp6 human adeno	243	19	100.0	91	2	07UDV7_RHOBA	07udv7 rhodospirill
171	19	100.0	80	2	05ICQ5_GADEN	05icq5 human adeno	244	19	100.0	91	2	092HJ5_RICCN	092hj5 rickettsia
172	19	100.0	80	2	05ICR9_GADEN	05icr9 human adeno	245	19	100.0	92	2	029222_PIG	029222 sus scrofa
173	19	100.0	80	2	05ICG0_GADEN	05icg0 human adeno	246	19	100.0	92	2	05W306_SIRCO	05w306 silene cont
174	19	100.0	80	2	05ICG4_GADEN	05icg4 human adeno	247	19	100.0	92	2	05W4F6_BACSK	05w4f6 bacillus cl
175	19	100.0	80	2	05ICR0_GADEN	05icr0 human adeno	248	19	100.0	92	2	05ICR3_GADEN	05icr3 human adeno
176	19	100.0	80	2	05ICR2_GADEN	05icr2 human adeno	249	19	100.0	93	2	06W4Q5_VIBAN	06w4q5 vibrio angu
177	19	100.0	81	2	096183_PLAF7	096183 plasmidium	250	19	100.0	93	2	09B8C4_PPASS	09b8c4 toxostoma c

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:24:34 ; Search time 38 Seconds
(Without alignments)
10.128 Million cell updates/sec

Title: US-10-825-958-13
Perfect score: 19
Sequence: 1 KLVF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

PIR 80:*
1: Dirl:*
2: Dirl:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	16	2 F41289	T-cell receptor al
2	19	100.0	26	2 G32502	T-cell receptor de
3	19	100.0	29	2 C47719	T-cell receptor al
4	19	100.0	30	2 B31461	T-cell receptor de
5	19	100.0	31	2 F31461	T-cell receptor de
6	19	100.0	32	2 A32502	T-cell receptor de
7	19	100.0	32	2 D32502	T-cell receptor de
8	19	100.0	32	2 D31461	T-cell receptor de
9	19	100.0	33	2 A31461	T-cell receptor de
10	19	100.0	33	2 E32502	T-cell receptor de
11	19	100.0	33	2 B32540	T-cell receptor de
12	19	100.0	33	2 I31461	T-cell receptor de
13	19	100.0	33	2 B31461	T-cell receptor de
14	19	100.0	33	2 S23094	beta-amyloid prote
15	19	100.0	34	2 C31461	T-cell receptor de
16	19	100.0	34	2 H31461	T-cell receptor de
17	19	100.0	34	2 I32502	T-cell receptor de
18	19	100.0	36	2 C32502	T-cell receptor de
19	19	100.0	36	2 H32502	T-cell receptor de
20	19	100.0	36	2 A32540	T-cell receptor de
21	19	100.0	42	2 PN0512	beta-amyloid prote
22	19	100.0	47	2 PC4133	hypothetical 47 pr
23	19	100.0	53	2 PS0009	glycyltin Alabib pr
24	19	100.0	57	2 A60045	Alzheimer's diseas
25	19	100.0	57	2 F60045	Alzheimer's diseas
26	19	100.0	57	2 D60045	Alzheimer's diseas
27	19	100.0	57	2 E60045	Alzheimer's diseas
28	19	100.0	57	2 G60045	Alzheimer's diseas
29	19	100.0	57	2 B60045	Alzheimer's diseas

30	19	100.0	57	2 D97742	hypothetical prote
31	19	100.0	67	2 B97758	hypothetical prote
32	19	100.0	69	2 T46201	protein translocat
33	19	100.0	69	2 B31979	peptidyl-di-peptida
34	19	100.0	71	2 AB2884	hypothetical prote
35	19	100.0	72	2 S28793	major merzoxite su
36	19	100.0	73	2 A38883	T-cell receptor al
37	19	100.0	75	2 S35774	hypothetical prote
38	19	100.0	78	2 B84305	hypothetical prote
39	19	100.0	79	2 C97829	hypothetical prote
40	19	100.0	81	2 H71614	protein translocat
41	19	100.0	82	2 PQ0438	Alzheimer's diseas
42	19	100.0	83	2 AD2896	hypothetical prote
43	19	100.0	84	2 AC3376	hypothetical prote
44	19	100.0	86	1 C64322	ribosomal protein
45	19	100.0	86	2 B44530	T-cell receptor al
46	19	100.0	90	2 H84410	hypothetical prote
47	19	100.0	90	2 D82760	hypothetical prote
48	19	100.0	91	2 E64413	hypothetical prote
49	19	100.0	91	2 H97796	RP534 protein homo
50	19	100.0	94	2 S61934	signal peptidase 1
51	19	100.0	95	1 BORR3	prostatic steroid
52	19	100.0	96	2 T25103	hypothetical prote
53	19	100.0	97	2 D64600	conserved hypochet
54	19	100.0	97	2 C71913	hypothetical prote
55	19	100.0	99	2 F95064	ribosomal protein
56	19	100.0	99	2 H97931	conserved hypochet
57	19	100.0	100	2 F83836	transcription regu
58	19	100.0	100	2 AF0773	hypothetical prote
59	19	100.0	101	2 A11753	Orf47 [bacterioph
60	19	100.0	105	2 S42212	hydroxymethylgluta
61	19	100.0	105	2 S17345	hydroxymethylgluta
62	19	100.0	106	2 S43069	hypothetical prote
63	19	100.0	107	2 F86869	hypothetical prote
64	19	100.0	109	1 A44275	nonstructural prot
65	19	100.0	109	1 MN1HB2	nonstructural prot
66	19	100.0	109	2 S58186	nonstructural prot
67	19	100.0	109	2 S58182	nonstructural prot
68	19	100.0	110	2 A24092	T-cell receptor al
69	19	100.0	110	2 A11856	hypothetical prote
70	19	100.0	110	2 A24444	hypothetical prote
71	19	100.0	112	2 S73078	hypothetical prote
72	19	100.0	112	2 T47326	T cell receptor al
73	19	100.0	113	4 I39320	hypothetical prote
74	19	100.0	116	2 F72419	hypothetical prote
75	19	100.0	116	2 E90716	hypothetical prote
76	19	100.0	116	2 T05517	absorbic acid-indu
77	19	100.0	117	2 H71431	hypothetical prote
78	19	100.0	117	2 T13210	minor capsid prote
79	19	100.0	119	2 AC0080	probable dihydron
80	19	100.0	120	2 AE0892	dihydroneopterin a
81	19	100.0	120	2 C26945	T-cell receptor de
82	19	100.0	121	2 S23781	insertion sequence
83	19	100.0	122	1 S58649	ribosomal protein
84	19	100.0	122	2 AG1887	hypothetical prote
85	19	100.0	122	2 E84154	cadmium-binding pr
86	19	100.0	122	2 S73009	hypothetical prote
87	19	100.0	123	1 H65093	probable dihydron
88	19	100.0	123	2 D85966	probable kinase yg
89	19	100.0	123	2 E91121	probable kinase [1
90	19	100.0	123	2 PL0032	T-cell receptor de
91	19	100.0	124	2 A70873	probable trxa prot
92	19	100.0	126	2 H69767	cytochrome-c oxida
93	19	100.0	127	1 CCR22V	cytochrome c2 prec
94	19	100.0	128	2 G86629	hypothetical prote
95	19	100.0	128	2 AC3428	transposase BMB14
96	19	100.0	129	2 S78103	T-cell receptor de
97	19	100.0	130	2 D29774	T-cell receptor al
98	19	100.0	131	2 B24092	T-cell receptor al
99	19	100.0	131	2 E24092	T-cell receptor al
100	19	100.0	133	2 S49487	long-chain-fatty-a
101	19	100.0	133	2 S57886	T cell receptor al
102	19	100.0	133	2 G45893	T-cell receptor al

103	19	100.0	134	2	S57890	T cell receptor Hw	176	19	100.0	190	2	A59418	kuntz type subc11
104	19	100.0	135	2	T13489	T-cell receptor al	177	19	100.0	190	2	G85542	glycoprotein/poly
105	19	100.0	136	2	C90254	hypothetical prote	178	19	100.0	190	2	G90692	glycoprotein/poly
106	19	100.0	137	2	S03477	T-cell receptor al	179	19	100.0	190	2	B64775	probable lipoprote
107	19	100.0	139	2	A70426	8-OXO-dGTPase doma	180	19	100.0	191	2	C64376	membrane protein h
108	19	100.0	140	2	B95049	hypothetical prote	181	19	100.0	191	2	E30754	hypothetical prote
109	19	100.0	140	2	H97919	(3R)-hydroxymyrist	182	19	100.0	191	2	E85607	probable tellurium
110	19	100.0	141	2	PL0045	T-cell receptor al	183	19	100.0	191	2	D90798	probable tellurium
111	19	100.0	142	2	D95237	phosphotyrosine pr	184	19	100.0	193	1	RDBPT4	dihydrofolate redu
112	19	100.0	142	2	E98101	conserved hypochet	185	19	100.0	193	2	T29706	hypothetical prote
113	19	100.0	142	2	D75134	hypothetical prote	186	19	100.0	194	2	T50787	hypothetical prote
114	19	100.0	143	2	JI0082	T-cell receptor de	187	19	100.0	194	2	S21859	hypothetical prote
115	19	100.0	144	2	B30471	hypothetical prote	188	19	100.0	194	2	F64025	hypothetical prote
116	19	100.0	144	2	AC6732	hypothetical prote	189	19	100.0	198	2	S39543	GTP-binding protei
117	19	100.0	144	2	AC2572	hypothetical prote	190	19	100.0	198	2	F95139	hemolysin A, proba
118	19	100.0	146	2	B64246	ribosomal protein	191	19	100.0	199	2	B67556	tellurium resistan
119	19	100.0	146	2	B97426	flagellar protein	192	19	100.0	199	2	PQ0542	polyprotein - suga
120	19	100.0	146	2	AH2258	hypothetical prote	193	19	100.0	199	2	H72242	flagellar L-ring p
121	19	100.0	147	2	S76050	hypothetical prote	194	19	100.0	199	2	T20927	hypothetical prote
122	19	100.0	152	2	F86473	hypothetical prote	195	19	100.0	201	2	S12789	GTP-binding protei
123	19	100.0	152	2	T06645	hypothetical prote	196	19	100.0	201	2	C97074	telurium resistan
124	19	100.0	156	1	B64021	hypothetical prote	197	19	100.0	201	2	F69988	hypothetical prote
125	19	100.0	157	2	E97424	hypothetical prote	198	19	100.0	202	2	S21346	probable pol polyp
126	19	100.0	157	2	AD2642	conserved hypochet	199	19	100.0	203	2	JO1091	trypsin inhibitor
127	19	100.0	158	2	E86191	hypothetical prote	200	19	100.0	203	2	T02868	GTP-binding protei
128	19	100.0	159	2	AF1372	hypothetical prote	201	19	100.0	203	2	T24042	trypsin inhibitor
129	19	100.0	159	2	AD1742	protein involved i	202	19	100.0	204	2	JO1092	trypsin inhibitor
130	19	100.0	159	2	A64672	hypothetical prote	203	19	100.0	204	2	S70149	DNA-invertase - Xa
131	19	100.0	159	2	H71845	hypothetical prote	204	19	100.0	204	2	T45948	hypothetical prote
132	19	100.0	159	2	H83279	hypothetical prote	205	19	100.0	205	2	S31127	GTP-binding protei
133	19	100.0	160	2	H83673	PTS system, galact	206	19	100.0	205	2	T34375	hypothetical prote
134	19	100.0	160	2	AE1485	hypothetical prote	207	19	100.0	206	2	JC7311	20K protein - soyb
135	19	100.0	162	2	AB2644	flagellar protein	208	19	100.0	207	2	T50814	GTP-binding protei
136	19	100.0	164	2	H64669	ribosomal protein	209	19	100.0	207	2	H84610	probable GTP-bind
137	19	100.0	164	2	D71846	chiot peroxidase f	210	19	100.0	207	2	T08520	DNA-invertase - En
138	19	100.0	165	2	D90600	hypothetical prote	211	19	100.0	207	2	S32180	DNA-invertase - Kl
139	19	100.0	165	2	H97142	baie 19.5K protein	212	19	100.0	208	2	AF3538	uracil phosphoribo
140	19	100.0	166	2	D37844	hypothetical prote	213	19	100.0	208	2	S49196	Kuntz trypsin inh
141	19	100.0	166	2	D87664	hypothetical prote	214	19	100.0	208	2	G34323	GTP-binding protei
142	19	100.0	167	2	A32646	peroxisomal membra	215	19	100.0	208	2	T03627	GTP-binding protei
143	19	100.0	169	2	E86502	ct303 hypothetical	216	19	100.0	208	2	T01588	GTP-binding protei
144	19	100.0	169	2	E70219	hypothetical prote	217	19	100.0	208	2	F64244	ATP synthase B cha
145	19	100.0	169	2	D90720	hypothetical prote	218	19	100.0	208	2	D64380	conserved hypochet
146	19	100.0	169	2	B85571	hypothetical prote	219	19	100.0	208	2	D88961	uracil phosphoribo
147	19	100.0	169	2	B64806	hypothetical prote	220	19	100.0	209	2	AI3292	uracil phosphoribo
148	19	100.0	169	2	PC4143	hypothetical 169 p	221	19	100.0	209	2	C97375	uracil phosphoribo
149	19	100.0	170	2	E81375	hypothetical prote	222	19	100.0	209	2	C87530	uracil phosphoribo
150	19	100.0	171	2	E70219	hypothetical prote	223	19	100.0	209	2	D95186	conserved hypochet
151	19	100.0	171	2	PC2038	smoach muscle proc	224	19	100.0	209	2	E98053	hypothetical prote
152	19	100.0	171	2	B87628	conserved hypochet	225	19	100.0	210	2	B87640	conserved hypochet
153	19	100.0	171	2	P90266	hypothetical prote	226	19	100.0	210	2	A85018	probable copper-co
154	19	100.0	171	2	D81278	probable periplasm	227	19	100.0	214	2	T06095	GTP-binding protei
155	19	100.0	173	2	C81549	conserved hypochet	228	19	100.0	214	2	T47892	hypothetical prote
156	19	100.0	175	2	G96535	hypothetical prote	229	19	100.0	214	2	JC7899	glutathione transf
157	19	100.0	176	1	A44056	22K protein - feil	230	19	100.0	215	2	S74602	hypothetical prote
158	19	100.0	176	2	A99234	dUDP-4-dehydrotham	231	19	100.0	215	2	F72412	hypothetical prote
159	19	100.0	176	2	G90357	dUDP-4-dehydrotham	232	19	100.0	216	2	JO0968	trypsin inhibitor
160	19	100.0	176	2	T22614	hypothetical prote	233	19	100.0	216	2	AF1513	probable transaldo
161	19	100.0	179	2	S64843	hypothetical prote	234	19	100.0	216	2	T50314	probable human pop
162	19	100.0	181	1	TI5YC	trypsin inhibitor	235	19	100.0	217	1	TI5Y	trypsin inhibitor
163	19	100.0	181	1	TI5YB	trypsin inhibitor	236	19	100.0	217	2	S19190	GTP-binding protei
164	19	100.0	181	2	T36787	probable NTP pyrop	237	19	100.0	217	2	AG3623	GTP-binding protei
165	19	100.0	182	2	E75597	probable lipopolys	238	19	100.0	217	2	F97405	GTP-binding protei
166	19	100.0	182	2	T40976	hypothetical prote	239	19	100.0	219	2	A64043	uracil-DNA glycosy
167	19	100.0	183	2	UX0311	kuntz type subc11	240	19	100.0	220	1	A33872	mitoculin precurs
168	19	100.0	183	2	S76453	hypothetical prote	241	19	100.0	220	2	H81048	biopolymer transpo
169	19	100.0	186	2	T06911	H-transporing tw	242	19	100.0	220	2	C87601	glutathione S-tran
170	19	100.0	186	2	T50672	probable zinc fing	243	19	100.0	222	2	T26213	hypothetical prote
171	19	100.0	187	2	F71063	protein F07G6.7 [i	244	19	100.0	224	1	MMWZRI	26.3K late gene tr
172	19	100.0	189	2	G89468	conserved hypochet	245	19	100.0	224	2	F71934	molybdenum ABC tran
173	19	100.0	189	2	AE0560	kuntz type subc11	246	19	100.0	224	2	B64579	molybdenum ABC tra
174	19	100.0	190	2	UX0310	kuntz type subc11	247	19	100.0	224	2	C36848	AZL protein - vari
175	19	100.0	190	2	A59416	kuntz type subc11	248	19	100.0	224	2	G72163	AZL protein - vari

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:30:14 ; Search time 50 Seconds

(without alignments)
7.002 Million cell updates/sec

Title: US-10-825-958-13

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: Issued Patents_AA.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/5/COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/6/COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/7/COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/H/COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS/COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE/COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	2	US-08-970-833-1
2	19	100.0	4	2	US-08-664-379B-17
3	19	100.0	4	2	US-09-095-106A-25
4	19	100.0	4	2	US-09-747-408-6
5	19	100.0	4	2	US-09-747-408-14
6	19	100.0	5	1	US-08-127-904-15
7	19	100.0	5	1	US-08-612-785B-10
8	19	100.0	5	2	US-08-970-833-2
9	19	100.0	5	2	US-08-703-675C-46
10	19	100.0	5	2	US-09-242-724-25
11	19	100.0	5	2	US-09-242-724-26
12	19	100.0	5	2	US-08-617-267C-10
13	19	100.0	5	2	US-08-617-267C-37
14	19	100.0	5	2	US-09-095-106A-1
15	19	100.0	5	2	US-09-095-106A-19
16	19	100.0	5	2	US-09-095-106A-43
17	19	100.0	5	2	US-09-747-408-8
18	19	100.0	5	2	US-09-747-408-16
19	19	100.0	5	5	PCT-US94-10475-15
20	19	100.0	6	1	US-08-612-785B-8
21	19	100.0	6	1	US-08-612-785B-9
22	19	100.0	6	1	US-08-612-785B-11
23	19	100.0	6	2	US-08-664-379B-19
24	19	100.0	6	2	US-08-703-675C-31
25	19	100.0	6	2	US-08-703-675C-32
26	19	100.0	6	2	US-08-703-675C-44

27	19	100.0	6	2	US-09-242-724-24	Sequence 24, Appl
28	19	100.0	6	2	US-09-242-724-27	Sequence 27, Appl
29	19	100.0	6	2	US-09-242-724-30	Sequence 30, Appl
30	19	100.0	6	2	US-09-242-724-31	Sequence 31, Appl
31	19	100.0	6	2	US-09-242-724-33	Sequence 33, Appl
32	19	100.0	6	2	US-08-617-267C-8	Sequence 8, Appl
33	19	100.0	6	2	US-08-617-267C-9	Sequence 9, Appl
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35	19	100.0	6	2	US-08-617-267C-43	Sequence 43, Appl
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37	19	100.0	6	2	US-09-095-106A-15	Sequence 15, Appl
38	19	100.0	6	2	US-09-747-408-11	Sequence 11, Appl
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44	19	100.0	7	2	US-08-703-675C-29	Sequence 29, Appl
45	19	100.0	7	2	US-08-703-675C-30	Sequence 30, Appl
46	19	100.0	7	2	US-08-617-267C-6	Sequence 6, Appl
47	19	100.0	7	2	US-08-617-267C-7	Sequence 7, Appl
48	19	100.0	7	2	US-09-242-709A-13	Sequence 13, Appl
49	19	100.0	7	2	US-09-095-106A-11	Sequence 11, Appl
50	19	100.0	7	2	US-09-095-106A-12	Sequence 12, Appl
51	19	100.0	7	2	US-09-747-408-2	Sequence 2, Appl
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53	19	100.0	7	2	US-09-747-408-19	Sequence 19, Appl
54	19	100.0	7	5	PCT-US94-10475-14	Sequence 14, Appl
55	19	100.0	8	1	US-08-457-804-1	Sequence 1, Appl
56	19	100.0	8	1	US-08-457-804-6	Sequence 6, Appl
57	19	100.0	8	1	US-08-457-804-7	Sequence 7, Appl
58	19	100.0	8	1	US-08-612-785B-5	Sequence 5, Appl
59	19	100.0	8	1	US-08-630-645-1	Sequence 1, Appl
60	19	100.0	8	2	US-08-703-675C-28	Sequence 28, Appl
61	19	100.0	8	2	US-08-617-267C-5	Sequence 5, Appl
62	19	100.0	8	2	US-09-095-106A-8	Sequence 8, Appl
63	19	100.0	8	2	US-09-095-106A-9	Sequence 9, Appl
64	19	100.0	8	2	US-08-766-596A-44	Sequence 44, Appl
65	19	100.0	8	2	US-08-766-596A-53	Sequence 53, Appl
66	19	100.0	8	2	US-09-668-314C-73	Sequence 73, Appl
67	19	100.0	8	5	PCT-US96-10220-1	Sequence 1, Appl
68	19	100.0	9	2	US-09-242-709A-4	Sequence 4, Appl
69	19	100.0	9	2	US-09-095-106A-6	Sequence 6, Appl
70	19	100.0	9	2	US-09-095-106A-7	Sequence 7, Appl
71	19	100.0	9	2	US-08-766-596A-54	Sequence 54, Appl
72	19	100.0	9	2	US-08-766-596A-64	Sequence 64, Appl
73	19	100.0	9	2	US-09-747-408-20	Sequence 20, Appl
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77	19	100.0	10	2	US-09-724-961-19	Sequence 19, Appl
78	19	100.0	10	2	US-09-724-961-20	Sequence 20, Appl
79	19	100.0	10	2	US-09-724-961-21	Sequence 21, Appl
80	19	100.0	10	2	US-09-724-961-22	Sequence 22, Appl
81	19	100.0	10	2	US-09-724-961-23	Sequence 23, Appl
82	19	100.0	10	2	US-09-724-961-24	Sequence 24, Appl
83	19	100.0	10	2	US-09-580-018-18	Sequence 18, Appl
84	19	100.0	10	2	US-09-580-018-19	Sequence 19, Appl
85	19	100.0	10	2	US-09-580-018-20	Sequence 20, Appl
86	19	100.0	10	2	US-09-580-018-21	Sequence 21, Appl
87	19	100.0	10	2	US-09-580-018-22	Sequence 22, Appl
88	19	100.0	10	2	US-09-580-018-23	Sequence 23, Appl
89	19	100.0	10	2	US-09-580-018-24	Sequence 24, Appl
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92	19	100.0	10	2	US-09-724-551-20	Sequence 20, Appl
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97	19	100.0	10	2	US-09-724-940-18	Sequence 18, Appl
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99	19	100.0	10	2	US-09-724-940-19	Sequence 19, Appl

100	19	100.0	10	2	US-09-724-940-20	Sequence 20, Appl	173	19	100.0	23	1	US-08-505-486-75	Sequence 75, Appl
101	19	100.0	10	2	US-09-724-940-21	Sequence 21, Appl	174	19	100.0	23	2	US-08-801-028-75	Sequence 75, Appl
102	19	100.0	10	2	US-09-724-940-22	Sequence 22, Appl	175	19	100.0	23	2	US-09-340-154-75	Sequence 75, Appl
103	19	100.0	10	2	US-09-724-940-23	Sequence 23, Appl	176	19	100.0	23	5	US-09-482-611B-75	Sequence 75, Appl
104	19	100.0	10	2	US-09-724-940-24	Sequence 24, Appl	177	19	100.0	23	5	PCT-US95-09338-75	Sequence 75, Appl
105	19	100.0	11	1	US-08-630-640-14	Sequence 14, Appl	178	19	100.0	23	5	PCT-US95-09339-75	Sequence 75, Appl
106	19	100.0	11	2	US-08-970-833-8	Sequence 8, Appl	179	19	100.0	26	1	US-08-304-585-7	Sequence 11, Appl
107	19	100.0	11	2	US-08-766-596A-14	Sequence 14, Appl	180	19	100.0	27	1	US-08-141-324-11	Sequence 11, Appl
108	19	100.0	11	2	US-08-766-596A-68	Sequence 68, Appl	181	19	100.0	27	1	US-08-141-324-12	Sequence 12, Appl
109	19	100.0	11	2	US-09-988-842-9	Sequence 9, Appl	182	19	100.0	27	1	US-08-541-902-11	Sequence 11, Appl
110	19	100.0	11	2	US-09-988-842-25	Sequence 25, Appl	183	19	100.0	27	1	US-08-541-902-12	Sequence 12, Appl
111	19	100.0	11	2	US-09-623-548A-957	Sequence 957, App	184	19	100.0	27	1	US-08-505-486-76	Sequence 76, Appl
112	19	100.0	11	2	US-09-623-548A-963	Sequence 963, App	185	19	100.0	27	1	US-08-505-486-77	Sequence 77, Appl
113	19	100.0	11	2	US-09-623-548A-990	Sequence 990, App	186	19	100.0	27	2	US-08-801-028-76	Sequence 76, Appl
114	19	100.0	11	2	US-09-657-276-957	Sequence 957, App	187	19	100.0	27	2	US-08-801-028-77	Sequence 77, Appl
115	19	100.0	11	2	US-09-657-276-963	Sequence 963, App	188	19	100.0	27	2	US-08-963-121C-9	Sequence 9, Appl
116	19	100.0	11	2	US-09-657-276-990	Sequence 990, App	189	19	100.0	27	2	US-09-340-154-76	Sequence 76, Appl
117	19	100.0	11	5	PCT-US96-10220-14	Sequence 14, Appl	190	19	100.0	27	2	US-09-340-154-77	Sequence 77, Appl
118	19	100.0	14	2	US-09-594-366-5	Sequence 5, Appl	191	19	100.0	27	2	US-09-543-513-9	Sequence 9, Appl
119	19	100.0	14	2	US-09-443-199C-1217	Sequence 1217, Ap	192	19	100.0	27	2	US-09-482-611B-76	Sequence 76, Appl
120	19	100.0	14	2	US-09-992-800-5	Sequence 5, Appl	193	19	100.0	27	2	US-09-482-611B-77	Sequence 77, Appl
121	19	100.0	15	1	US-08-480-190-39	Sequence 39, Appl	194	19	100.0	27	5	PCT-US95-04803-10	Sequence 10, Appl
122	19	100.0	15	1	US-08-612-785B-4	Sequence 4, Appl	195	19	100.0	27	5	PCT-US95-09338-76	Sequence 76, Appl
123	19	100.0	15	1	US-08-612-785B-14	Sequence 14, Appl	196	19	100.0	27	5	PCT-US95-09338-77	Sequence 77, Appl
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125	19	100.0	15	1	US-08-488-379-39	Sequence 39, Appl	198	19	100.0	27	5	PCT-US95-09339-77	Sequence 77, Appl
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129	19	100.0	15	2	US-08-766-596A-58	Sequence 58, Appl	202	19	100.0	28	1	US-08-986-948-7	Sequence 7, Appl
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131	19	100.0	15	2	US-08-766-596A-61	Sequence 61, Appl	204	19	100.0	28	1	US-08-461-216-4	Sequence 2, Appl
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139	19	100.0	17	2	US-09-594-366-3	Sequence 3, Appl	212	19	100.0	28	2	US-09-388-890-9	Sequence 9, Appl
140	19	100.0	17	2	US-09-623-548A-950	Sequence 950, App	213	19	100.0	28	2	US-09-388-890-10	Sequence 10, Appl
141	19	100.0	17	2	US-09-623-548A-983	Sequence 983, App	214	19	100.0	28	2	US-09-388-890-12	Sequence 12, Appl
142	19	100.0	17	2	US-09-929-800-3	Sequence 3, Appl	215	19	100.0	28	2	US-09-388-890-13	Sequence 13, Appl
143	19	100.0	17	2	US-09-657-276-950	Sequence 950, App	216	19	100.0	28	2	US-09-388-890-14	Sequence 14, Appl
144	19	100.0	17	2	US-09-657-276-983	Sequence 983, App	217	19	100.0	28	2	US-09-264-709A-1	Sequence 1, Appl
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155	19	100.0	19	2	US-09-724-551-75	Sequence 75, Appl	228	19	100.0	28	2	US-09-660-954-12	Sequence 12, Appl
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160	19	100.0	19	2	US-10-815-391-5	Sequence 5, Appl	233	19	100.0	28	2	US-09-623-548A-965	Sequence 965, App
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162	19	100.0	19	2	US-09-724-940-75	Sequence 75, Appl	235	19	100.0	28	2	US-09-623-548A-992	Sequence 992, App
163	19	100.0	19	2	US-10-934-609-5	Sequence 5, Appl	236	19	100.0	28	2	US-09-623-548A-1003	Sequence 1003, App
164	19	100.0	19	2	US-10-884-882-5	Sequence 5, Appl	237	19	100.0	28	2	US-09-657-276-959	Sequence 959, App
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166	19	100.0	19	3	US-10-816-404-5	Sequence 5, Appl	239	19	100.0	28	2	US-09-657-276-976	Sequence 976, App
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172	19	100.0	20	2	US-09-585-817-33	Sequence 33, Appl	245	19	100.0	30	1	US-08-609-090-3	Sequence 3, Appl

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:30:23 ; Search time 182 Seconds
(without alignments)
10.181 Million cell updates/sec

Title: US-10-825-958-13

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	19	100.0	4	3	US-09-867-847-15	Sequence 15, Appl
2	19	100.0	4	3	US-09-867-847-23	Sequence 23, Appl
3	19	100.0	4	3	US-09-850-061A-25	Sequence 25, Appl
4	19	100.0	4	3	US-09-915-092-5	Sequence 5, Appl
5	19	100.0	4	3	US-09-915-092-13	Sequence 13, Appl
6	19	100.0	4	3	US-09-747-408-6	Sequence 6, Appl
7	19	100.0	4	3	US-09-747-408-14	Sequence 14, Appl
8	19	100.0	4	3	US-10-721-774-25	Sequence 25, Appl
9	19	100.0	4	5	US-10-728-028-5	Sequence 5, Appl
10	19	100.0	4	5	US-10-728-028-13	Sequence 13, Appl
11	19	100.0	4	5	US-10-825-958-13	Sequence 13, Appl
12	19	100.0	4	5	US-10-825-958-21	Sequence 21, Appl
13	19	100.0	4	5	US-10-666-095-2	Sequence 2, Appl
14	19	100.0	5	3	US-09-867-847-17	Sequence 17, Appl
15	19	100.0	5	3	US-09-867-847-25	Sequence 25, Appl
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100	19	100.0	7	5	US-10-505-313-267	Sequence 267, App

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114	19	100.0	8	5	US-10-817-979-73	Sequence 73, App	187	19	100.0	10	5	US-10-890-071-18	Sequence 18, Appl
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135	19	100.0	10	3	US-09-573-822C-628	Sequence 628, App	208	19	100.0	10	5	US-10-928-926-24	Sequence 24, Appl
136	19	100.0	10	4	US-10-741-204-35	Sequence 35, Appl	209	19	100.0	10	6	US-11-058-757-18	Sequence 18, Appl
137	19	100.0	10	4	US-10-741-204-43	Sequence 43, Appl	210	19	100.0	10	6	US-11-058-757-19	Sequence 19, Appl
138	19	100.0	10	4	US-10-741-205-3	Sequence 3, Appl	211	19	100.0	10	6	US-11-058-757-20	Sequence 20, Appl
139	19	100.0	10	4	US-10-741-205-8	Sequence 8, Appl	212	19	100.0	10	6	US-11-058-757-21	Sequence 21, Appl
140	19	100.0	10	4	US-10-741-205-13	Sequence 13, Appl	213	19	100.0	10	6	US-11-058-757-22	Sequence 22, Appl
141	19	100.0	10	4	US-10-741-208-35	Sequence 35, Appl	214	19	100.0	10	6	US-11-058-757-23	Sequence 23, Appl
142	19	100.0	10	4	US-10-721-774-2	Sequence 2, Appl	215	19	100.0	10	6	US-11-058-757-24	Sequence 24, Appl
143	19	100.0	10	5	US-10-889-999-18	Sequence 18, Appl	216	19	100.0	10	6	US-11-207-954-1	Sequence 1, Appl
144	19	100.0	10	5	US-10-889-999-19	Sequence 19, Appl	217	19	100.0	11	3	US-09-988-842-9	Sequence 9, Appl
145	19	100.0	10	5	US-10-889-999-20	Sequence 20, Appl	218	19	100.0	11	3	US-09-988-842-25	Sequence 25, Appl
146	19	100.0	10	5	US-10-889-999-21	Sequence 21, Appl	219	19	100.0	11	4	US-10-235-483-14	Sequence 14, Appl
147	19	100.0	10	5	US-10-889-999-22	Sequence 22, Appl	220	19	100.0	11	4	US-10-235-483-68	Sequence 68, Appl
148	19	100.0	10	5	US-10-889-999-23	Sequence 23, Appl	221	19	100.0	11	4	US-10-050-200-33	Sequence 33, Appl
149	19	100.0	10	5	US-10-889-999-24	Sequence 24, Appl	222	19	100.0	11	4	US-10-423-047-3	Sequence 3, Appl
150	19	100.0	10	5	US-10-890-070-18	Sequence 18, Appl	223	19	100.0	11	4	US-10-237-673-20	Sequence 20, Appl
151	19	100.0	10	5	US-10-890-070-19	Sequence 19, Appl	224	19	100.0	11	4	US-10-741-204-41	Sequence 41, Appl
152	19	100.0	10	5	US-10-890-070-20	Sequence 20, Appl	225	19	100.0	11	4	US-10-741-205-39	Sequence 39, Appl
153	19	100.0	10	5	US-10-890-070-21	Sequence 21, Appl	226	19	100.0	11	4	US-10-741-208-41	Sequence 41, Appl
154	19	100.0	10	5	US-10-890-070-22	Sequence 22, Appl	227	19	100.0	11	5	US-10-464-117-13	Sequence 13, Appl
155	19	100.0	10	5	US-10-890-070-23	Sequence 23, Appl	228	19	100.0	11	5	US-10-772-230-9	Sequence 9, Appl
156	19	100.0	10	5	US-10-890-070-24	Sequence 24, Appl	229	19	100.0	11	5	US-10-772-230-25	Sequence 25, Appl
157	19	100.0	10	5	US-10-890-000-18	Sequence 18, Appl	230	19	100.0	11	5	US-10-625-854-135	Sequence 125, App
158	19	100.0	10	5	US-10-890-000-19	Sequence 19, Appl	231	19	100.0	11	5	US-10-625-854-138	Sequence 138, App
159	19	100.0	10	5	US-10-890-000-20	Sequence 20, Appl	232	19	100.0	11	6	US-11-066-697-957	Sequence 957, App
160	19	100.0	10	5	US-10-890-000-21	Sequence 21, Appl	233	19	100.0	11	6	US-11-066-697-963	Sequence 963, App
161	19	100.0	10	5	US-10-890-000-22	Sequence 22, Appl	234	19	100.0	11	6	US-11-066-697-990	Sequence 990, App
162	19	100.0	10	5	US-10-890-000-23	Sequence 23, Appl	235	19	100.0	11	6	US-11-291-770-20	Sequence 20, Appl
163	19	100.0	10	5	US-10-890-000-24	Sequence 24, Appl	236	19	100.0	12	3	US-09-867-847-8	Sequence 8, Appl
164	19	100.0	10	5	US-10-823-463-18	Sequence 18, Appl	237	19	100.0	12	3	US-10-810-881A-115	Sequence 115, App
165	19	100.0	10	5	US-10-823-463-19	Sequence 19, Appl	238	19	100.0	12	5	US-10-810-881A-117	Sequence 117, App
166	19	100.0	10	5	US-10-823-463-20	Sequence 20, Appl	239	19	100.0	12	5	US-10-508-586-2	Sequence 2, Appl
167	19	100.0	10	5	US-10-823-463-21	Sequence 21, Appl	240	19	100.0	12	5	US-10-508-586-3	Sequence 3, Appl
168	19	100.0	10	5	US-10-823-463-22	Sequence 22, Appl	241	19	100.0	12	5	US-10-625-854-113	Sequence 113, App
169	19	100.0	10	5	US-10-823-463-23	Sequence 23, Appl	242	19	100.0	12	5	US-10-625-854-136	Sequence 126, App
170	19	100.0	10	5	US-10-823-463-24	Sequence 24, Appl	243	19	100.0	12	5	US-10-625-854-139	Sequence 139, App
171	19	100.0	10	5	US-10-728-028-19	Sequence 19, Appl	244	19	100.0	12	5	US-10-945-133-2	Sequence 2, Appl
172	19	100.0	10	5	US-10-822-968-18	Sequence 18, Appl	245	19	100.0	12	5	US-10-945-133-3	Sequence 3, Appl
173	19	100.0	10	5	US-10-822-968-19	Sequence 19, Appl	246	19	100.0	12	6	US-11-012-797A-33	Sequence 33, Appl